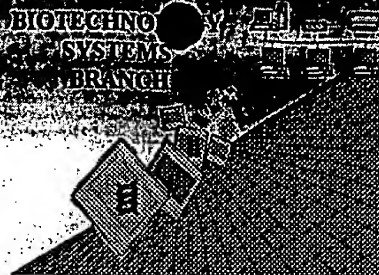The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/747,029_

Source: _OIPE_

Date Processed by STIC: _4/16/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u> <u>SUGGESTED CORRECTION</u>   SERIAL NUMBER: _09/747,029_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of "Artificial" (NEW RULES)
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 4/06/2001

OIPE

RAW SEQUENCE LISTING   DATE: 04/16/2001
PATENT APPLICATION: US/09/747,029   TIME: 17:23:51

Input Set : A:\PTO.txt
Output Set: N:\CRF3\04162001\I747029.raw

Does Not Comply
Corrected Diskette Needed
pp 1-2,4-5

```
 3 <110> APPLICANT: Union, Ann
 4        Moereels, Henri
 5        Meheus, Lydie
 7 <120> TITLE OF INVENTION: PEPTIDES DESIGNED FOR THE DIAGNOSIS AND TREATMENT OF RHEUMATOID
 8        ARTHRITIS
10 <130> FILE REFERENCE: 11362.0031NPUS00 INNS:031
12 <140> CURRENT APPLICATION NUMBER: US 09/747,029
13 <141> CURRENT FILING DATE: 2000-12-21
15 <150> PRIOR APPLICATION NUMBER: EP 00870195.5
16 <151> PRIOR FILING DATE: 2000-09-08
18 <150> PRIOR APPLICATION NUMBER: EP 99870280.7
19 <151> PRIOR FILING DATE: 1999-12-21
21 <160> NUMBER OF SEQ ID NOS: 22
23 <170> SOFTWARE: PatentIn version 3.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 18
27 <212> TYPE: PRT
28 <213> ORGANISM: Artificial
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Synthetic Peptides
33 <220> FEATURE:
34 <221> NAME/KEY: MOD_RES
35 <222> LOCATION: (1)..(1)
36 <223> OTHER INFORMATION: Xaa represents Ser, Thr, Asp, Glu, Asn, Gln, His, Lys or Arg
39 <220> FEATURE:
40 <221> NAME/KEY: MOD_RES
41 <222> LOCATION: (2)..(2)
42 <223> OTHER INFORMATION: Xaa represents Ser, Thr, Asp, Glu, Asn, Gln, His, Lys or Arg
45 <220> FEATURE:
46 <221> NAME/KEY: MOD_RES
47 <222> LOCATION: (3)..(3)
48 <223> OTHER INFORMATION: Xaa represents Ser, Thr, Asp, Glu, Asn, Gln, His, Lys or Arg
51 <220> FEATURE:
52 <221> NAME/KEY: MOD_RES
53 <222> LOCATION: (4)..(4)
54 <223> OTHER INFORMATION: Xaa represents Ile, Leu, Val, Ala or Met
57 <220> FEATURE:
58 <221> NAME/KEY: MOD_RES
59 <222> LOCATION: (5)..(5)
60 <223> OTHER INFORMATION: Xaa represents His, Lys, Arg, Asp, Glu, Ser, Thr, Tyr, Phe or Trp
63 <220> FEATURE:
64 <221> NAME/KEY: MOD_RES
65 <222> LOCATION: (6)..(6)
66 <223> OTHER INFORMATION: Xaa represents Gly
69 <220> FEATURE:
70 <221> NAME/KEY: MOD_RES
71 <222> LOCATION: (7)..(7)
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C--> (line 28) *see item 11 on Error Summary Sheet*

RAW SEQUENCE LISTING   DATE: 04/16/2001
PATENT APPLICATION: US/09/747,029   TIME: 17:23:51

Input Set : A:\PTO.txt
Output Set: N:\CRF3\04162001\I747029.raw

```
 72 <223> OTHER INFORMATION: Xaa represents His, Lys, Arg, Asp, Glu, Ser, Thr, Tyr, Phe or Trp
 75 <220> FEATURE:
 76 <221> NAME/KEY: MOD_RES
 77 <222> LOCATION: (8)..(8)
 78 <223> OTHER INFORMATION: Xaa represents Pro or Gly
 81 <220> FEATURE:
 82 <221> NAME/KEY: MOD_RES
 83 <222> LOCATION: (10)..(10)
 84 <223> OTHER INFORMATION: Xaa represents Ser, Thr, Asp, Gly
 87 <220> FEATURE:
 88 <221> NAME/KEY: MOD_RES
 89 <222> LOCATION: (11)..(11)
 90 <223> OTHER INFORMATION: Xaa represents Cit, Gly, Ser or Thr
 93 <220> FEATURE:
 94 <221> NAME/KEY: MOD_RES
 95 <222> LOCATION: (12)..(12)
 96 <223> OTHER INFORMATION: Xaa represents Cit
 99 <220> FEATURE:
100 <221> NAME/KEY: MOD_RES
101 <222> LOCATION: (13)..(13)
102 <223> OTHER INFORMATION: Xaa represents Gly
105 <220> FEATURE:
106 <221> NAME/KEY: MOD_RES
107 <222> LOCATION: (14)..(14)
108 <223> OTHER INFORMATION: Xaa represents His, Lys, Arg, Asp, Glu, Ser, Thr, Tyr, Phe or Trp
111 <220> FEATURE:
112 <221> NAME/KEY: MOD_RES
113 <222> LOCATION: (15)..(15)
114 <223> OTHER INFORMATION: Xaa represent Arg, Lys, His, Asp, Glu, Ser, Thr, Gln, Asn, Tyr, P
115        he or Trp
118 <220> FEATURE:
119 <221> NAME/KEY: MOD_RES
120 <222> LOCATION: (17)..(17)
121 <223> OTHER INFORMATION: Xaa represents Gly
124 <220> FEATURE:
125 <221> NAME/KEY: MOD_RES
126 <222> LOCATION: (18)..(18)
127 <223> OTHER INFORMATION: Xaa represents Tyr, His, Lys, Arg, Asp, Glu, Ser, Thr, Gln, Asn,
128        Phe, Trp
131 <400> SEQUENCE: 1
133 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys
134 1                   5                  10                  15
136 Xaa Xaa
139 <210> SEQ ID NO: 2
140 <211> LENGTH: 15
141 <212> TYPE: PRT
142 <213> ORGANISM: Artificial
144 <220> FEATURE:
145 <223> OTHER INFORMATION: Synthetic Peptides
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RAW SEQUENCE LISTING   DATE: 04/16/2001
PATENT APPLICATION: US/09/747,029   TIME: 17:23:51

          Input Set : A:\PTO.txt
          Output Set: N:\CRF3\04162001\I747029.raw

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147 <220> FEATURE:
148 <221> NAME/KEY: MOD_RES
149 <222> LOCATION: (1)..(1)
150 <223> OTHER INFORMATION: Xaa represents Ile, Leu, Val, Ala or Met
153 <220> FEATURE:
154 <221> NAME/KEY: MOD_RES
155 <222> LOCATION: (2)..(2)
156 <223> OTHER INFORMATION: Xaa represents His, Lys, Arg, Asp, Glu, Ser, Thr, Tyr, Phe or Trp
159 <220> FEATURE:
160 <221> NAME/KEY: MOD_RES
161 <222> LOCATION: (3)..(3)
162 <223> OTHER INFORMATION: Xaa represents Gly
165 <220> FEATURE:
166 <221> NAME/KEY: MOD_RES
167 <222> LOCATION: (4)..(4)
168 <223> OTHER INFORMATION: Xaa represents His, Lys, Arg, Asp, Glu, Ser, Thr, Tyr, Phe or Trp
171 <220> FEATURE:
172 <221> NAME/KEY: MOD_RES
173 <222> LOCATION: (5)..(5)
174 <223> OTHER INFORMATION: Xaa represents Pro or Gly
177 <220> FEATURE:
178 <221> NAME/KEY: MOD_RES
179 <222> LOCATION: (7)..(7)
180 <223> OTHER INFORMATION: Xaa represents Ser, Thr, Asp or Gly
183 <220> FEATURE:
184 <221> NAME/KEY: MOD_RES
185 <222> LOCATION: (8)..(8)
186 <223> OTHER INFORMATION: Xaa represents Cit, Gly, Ser or Thr
189 <220> FEATURE:
190 <221> NAME/KEY: MOD_RES
191 <222> LOCATION: (9)..(9)
192 <223> OTHER INFORMATION: Xaa represents Cit
195 <220> FEATURE:
196 <221> NAME/KEY: MOD_RES
197 <222> LOCATION: (10)..(10)
198 <223> OTHER INFORMATION: Xaa represents Gly
201 <220> FEATURE:
202 <221> NAME/KEY: MOD_RES
203 <222> LOCATION: (11)..(11)
204 <223> OTHER INFORMATION: Xaa represents His, Lys, Arg, Asp, Glu, Ser, Thr, Tyr, Phe or Trp
207 <220> FEATURE:
208 <221> NAME/KEY: MOD_RES
209 <222> LOCATION: (12)..(12)
210 <223> OTHER INFORMATION: Xaa represents Arg, Lys, His, Asp, Glu, Ser, Thr, Gln, Asn, Tyr,
211       Phe or Trp
214 <220> FEATURE:
215 <221> NAME/KEY: MOD_RES
216 <222> LOCATION: (14)..(14)
217 <223> OTHER INFORMATION: Xaa represents Gly
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220 <220> FEATURE:
221 <221> NAME/KEY: MOD_RES
222 <222> LOCATION: (15)..(15)
223 <223> OTHER INFORMATION: Xaa represents Tyr, His, Lys, Arg, Asp, Glu, Ser, Thr, Gln, Asn,
224       Phe or Trp
227 <400> SEQUENCE: 2
229 Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
230 1               5                   10                  15
232 <210> SEQ ID NO: 3
233 <211> LENGTH: 14
234 <212> TYPE: PRT
235 <213> ORGANISM: Artificial
237 <220> FEATURE:
238 <223> OTHER INFORMATION: Synthetic Peptides
240 <220> FEATURE:
241 <221> NAME/KEY: MOD_RES
242 <222> LOCATION: (1)..(1)
243 <223> OTHER INFORMATION: Xaa represents His, Lys, Arg, Asp, Glu, Ser, Thr, Tyr, Phe or Trp
246 <220> FEATURE:
247 <221> NAME/KEY: MOD_RES
248 <222> LOCATION: (2)..(2)
249 <223> OTHER INFORMATION: Xaa represents Gly
252 <220> FEATURE:
253 <221> NAME/KEY: MOD_RES
254 <222> LOCATION: (3)..(3)
255 <223> OTHER INFORMATION: Xaa represents His, Lys, Arg, Asp, Glu, Ser, Thr, Tyr, Phe or Trp
258 <220> FEATURE:
259 <221> NAME/KEY: MOD_RES
260 <222> LOCATION: (4)..(4)
261 <223> OTHER INFORMATION: Xaa represents Pro or Gly
264 <220> FEATURE:
265 <221> NAME/KEY: MOD_RES
266 <222> LOCATION: (6)..(6)
267 <223> OTHER INFORMATION: Xaa represents Ser, Thr, Asp or Gly
270 <220> FEATURE:
271 <221> NAME/KEY: MOD_RES
272 <222> LOCATION: (7)..(7)
273 <223> OTHER INFORMATION: Xaa represents Cit, Gly, Ser or Thr
276 <220> FEATURE:
277 <221> NAME/KEY: MOD_RES
278 <222> LOCATION: (8)..(8)
279 <223> OTHER INFORMATION: Xaa represents Cit
282 <220> FEATURE:
283 <221> NAME/KEY: MOD_RES
284 <222> LOCATION: (9)..(9)
285 <223> OTHER INFORMATION: Xaa represents Gly
288 <220> FEATURE:
289 <221> NAME/KEY: MOD_RES
290 <222> LOCATION: (10)..(10)
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/747,029

DATE: 04/16/2001
TIME: 17:23:51

Input Set : A:\PTO.txt
Output Set: N:\CRF3\04162001\I747029.raw

```
291 <223> OTHER INFORMATION: Xaa represents His, Lys, Arg, Asp, Glu, Ser, Thr, Tyr, Phe or Trp
295 <220> FEATURE:
296 <221> NAME/KEY: MOD_RES
297 <222> LOCATION: (11)..(11)
298 <223> OTHER INFORMATION: Xaa represents Arg, Lys, His, Asp, Glu, Ser, Thr, Gln, Asn, Tyr,
299         Phe or Trp
302 <220> FEATURE:
303 <221> NAME/KEY: MOD_RES
304 <222> LOCATION: (13)..(13)
305 <223> OTHER INFORMATION: Xaa represents Gly
308 <220> FEATURE:
309 <221> NAME/KEY: MOD_RES
310 <222> LOCATION: (14)..(14)
311 <223> OTHER INFORMATION: Xaa represents Try His, Lys, Arg, Asp, Glu, Ser, Thr, Gln, Asn,
312         Phe or Trp
315 <400> SEQUENCE: 3
317 Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
318 1               5                       10
320 <210> SEQ ID NO: 4
321 <211> LENGTH: 18
322 <212> TYPE: PRT
323 <213> ORGANISM: Artificial
325 <220> FEATURE:
326 <223> OTHER INFORMATION: Synthetic Peptides
328 <220> FEATURE:
329 <221> NAME/KEY: MOD_RES
330 <222> LOCATION: (1)..(1)
331 <223> OTHER INFORMATION: Xaa represents Ser, Thr, Asp, Glu, Asn, Gln, His, Lys or Arg
334 <220> FEATURE:
335 <221> NAME/KEY: MOD_RES
336 <222> LOCATION: (2)..(2)
337 <223> OTHER INFORMATION: Xaa represents Ser, Thr, Asp, Glu, Asn, Gln, His, Lys or Arg
340 <220> FEATURE:
341 <221> NAME/KEY: MOD_RES
342 <222> LOCATION: (3)..(3)
343 <223> OTHER INFORMATION: Xaa represents Ser, Thr, Asp, Glu, Asn, Gln, His, Lys or Arg
346 <220> FEATURE:
347 <221> NAME/KEY: MOD_RES
348 <222> LOCATION: (4)..(4)
349 <223> OTHER INFORMATION: Xaa represents Ile, Leu, Val, Ala or Met
352 <220> FEATURE:
353 <221> NAME/KEY: MOD_RES
354 <222> LOCATION: (5)..(5)
355 <223> OTHER INFORMATION: Xaa represents His, Lys, Arg, Asp, Glu, Ser, Thr, Tyr, Phe or Trp
358 <220> FEATURE:
359 <221> NAME/KEY: MOD_RES
360 <222> LOCATION: (6)..(6)
361 <223> OTHER INFORMATION: Xaa represents Gly
364 <220> FEATURE:
```

W--> (line 317)
C--> (line 323)

Tyr? (handwritten annotation)

please correct this error in subsequent sequences, too (handwritten annotation)

FYI (handwritten annotation)

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields f each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 04/16/2001
PATENT APPLICATION: US/09/747,029   TIME: 17:23:52

Input Set : A:\PTO.txt
Output Set: N:\CRF3\04162001\I747029.raw

L:28 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:142 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:235 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:323 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:428 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:431 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:437 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:530 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:536 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:623 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:651 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:664 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:673 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:701 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:720 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:729 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:748 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:757 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:776 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:785 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:804 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:810 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:829 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:835 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:854 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:860 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:873 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:879 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:892 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:901 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:914 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:920 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:933 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:939 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:952 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:958 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:971 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:977 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:990 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22